GenCore version 5.11.3 Copyright (c) 1993 $-2003 - 6 \sin \rho \sin \rho \sin \rho \sin \rho$

OM protein - protein search, using sw model

Run on.

January 16, 2003, 16:42:17 ; Scarch time 8.23429 Seconds (without alignments) 58.517 Million cell updates/sec

US-09-856-070-18 24

1 KEELM 5 Perfect score: Sequence.

Gapop 10.0 , Gapext 0.5 SLOSMM62 Scoring table.

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR_73:* Database :

1: piri:* 2: pir2:* 3: pir3:*

4: pir4:*

Pred No is the compact for solds predicted by chare to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	- Ω			destrin rat	destrin (validated	destrin - piq		9R protein vario	2	A38R protein · var	EBV diversity of effect	Sall4R protein pre		in'erleukin-l-beta	hypothetical proto	hypothetical prote		hypothetical prote	probable ribosomal	arbG protein Erw	hypothetical CpG·i		farmesyltranstrans	hypothetical prote	hypothetical prote	lipoate-protein li	VHS domain contain	Probable coproport
SUMMARIES	Q1	B71487	AB1311	771846	H64669	JE0223	A54184	A35179	Aseron	128579	142520	272168	137420	JC1779	336852	IE2446	F75111	271022	727524	AH3161	P71180	A42603	138167	PC4304	A5.405.8	T06503	T05120	C90567	T39651	B71564
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C; Accession: B71487 P;Stephens, P.S.; K Science 282, 754-75 A, Fitle: Genome seq	sion: B7 ens, P.S 282, 75 . Genomo	C:Accession: B71487 P:Stephens, P.S.: Kalman, S. Science 282, 754-759, 1998 A.Fitte, Genome sequence of	si 4-	La c	.J.; Fan, J.	e, R.; Aravind, L.; Mitchelen of humans: Chlamydia t
A; Reference number: A A Accession: P71487 A; Status: preliminary A; Molecule type: LNA A; Pesidues: 1-97 < APA	sion: B7 sion: B7 s: preli ile type	A, Reference number: A71570. A, Accession: H71487 A, Status: preliminary A, Molecule type: LWA A, Pesidues: 1-97 - ARN		<u>=</u>	MULD**44000809; PMTD:9784136	
A, Cluss Tefet A) Expetimenta C)Genetics: A)Gene: CT656	refeten imental ics: CT656		ALÇOTS Seroty	. 9d. YP€	ALGOTATO, THE APPOINT AND GOODELE. Selotype D. Strain UM-3/CX	POTALARSTALSTON TELETOR
Query Match Best Local Matches		Similarity 100 5; Conservative	Vat	100.0%; 100.0%; ive	Score 24; DB 2; Length 97 	97; s 0: Caps 0;
oy du	1 KEELM 24 KEELM	4 5 2 8				

RESULT 2

Conserved hypotherical principal banded including the lingerical transfer and anytogenes (Species, Listeria monocytogenes)
C.Species. Listeria monocytogenes
C.Species. Listeria monocytogenes
C.Species. Listeria monocytogenes
C.Accession. AR131
E.Gaser, P. Frangeri, E. Buchrieser, C. Amend, A. Baquero, F., Berche, P., Blocc
C.Accession. AR131
E.Glaser, E. Frangeri, E. Buchrieser, C. Amend, A. Baquero, F., Berche, P., Blocc
C. Donard G., Duchaud, E., Durand, E., Dussauget, O.; Entian, K.D.; Fsihl,
D.: Tones, I. M.: Karst, W. Sinces, E., Kurapkat, C.; Madueno, E.; Maitournam, A.;
A.Authors: Kreft, J.: Kaho, M.: Kunst, F.; Kurapkat, C.; Madueno, E.; Maitournam, A.;
A.Title Comparetive genomics of Listeria species.
A.Fitle Comparetive genomics of Listeria species.
A.Recession. AB1311
A.Status, preliminary

A,Molecuie Eyper DNA A,Residues 1-121 (GLA) A,Chesidues 1-121 (GLA) A,Chesiduental source: MH N^_n0(\$)), FibW PAPPerus 1, Fib gladitots, Norw CROUT 7 A,Experimental source: Strain EGD:e C,Genetics:

Query Match

100.0%, Score 24, DB 2, Length 121;

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Anoto. sequence extracted from NCBI backbone (NCBINE13795), NCHIP-137954), NCHIP-137954, NCHIP-137954, NCHIP-137954, NCHIP-137956, NCHIP-13796, NCHIP-137966, NCHIP-137966, NCHIP-137966, NCHIP-137966, NCHIP-13796,
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(Species, Homo sapions (man))
(C)Species, Homo sapions (man)
(C)Species, Homo sapions (man)
(C)Species, AS4.84
(R)Hawkins, M.; Pope, B.; Maciver, S.K.; Weeds, A.G.
(R)Hawkins, M.; Pope, B.; Maciver, A.G.
(R)Hawins actin depolymentaling factor mediates a pH-sensitive destruction of act A; Reforence number: A54184; MUID:94002009; PMID:8399167
(A)Molecule Lype: mRNA
                                                                                                                                                                                                            ApDescription, Complete amino acid sequences and phosphorylation sites, determined by
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F:2/Modified site, actin binding #status predicted
F:3/Binding site: phosphate (Ser) (covalent) #status predicted
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A;Experimental source: fetal brain
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O
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Local Similarity 100.0%; Pred. No. 1.4e+02;
Nos 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                  A Reference number: JR9222
A; Accession: JE9223
A; Molecule type: protein
A; Residues: 1-164 < kAn>
C; Suporfamily: cofilin
C; Keywords: acetylated amino end; phosphoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                     C;Accession: JE0223
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%;
5; Conservative 0
                                                                                                                                                            submitted to JIPID, August 1998
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A;Cross-references: GDB:249179
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, F.D.; Smith, H.O.; Fraser, C. A;Ittle: The complete genome sequence of the gastric pathogen Helicohacter pylori
A;Retecence number: A64529; MUID:97394467; PMID:9252185
A;Acression: H64669
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rosidose, 1, 14.
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A;Cross-references- GH-AF000626; GH-AF000511; MID-92314360; DIDN;AAD08246.1; PID:9231436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiAlm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Javs, C.; Gibson, R.; Morborg, D.; Mills, S.D.; Llang, Q.; Taylor, D.R.; Vovis, G.P.; Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genomic sequence comparison of two unrelated isolates of the human qastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
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A:Cross-references: GB:AE001540; GB:AE001449; NID·q4155717; PIDN:AAD06701 1; PID:g415572
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C.Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #fext_change 13-Aug-1999
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C;Date: 21-Auq-1998 #sequence_revision 21-Auq-1998 #text_change 24 Nov 1999
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100.0%; Pred. No. le+02;
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                        117 KEELM 121
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NyAlternate names actin-depolymerizing factor
C.Species (dallus quilus (chicken)
C.Species (dallus quilus (chicken)
C.Species (dallus quilus (chicken)
C.Species (dallus quilus quilus (chicken)
C.Sacession: A35702, A35703, A40672
C.Sacession: A35702, A35703, A40672
R.Adams, M.E., Minamido, L.S., Duester, G.; Bamburg, J.R.
R.Adams, M.E., Minamido, L.S.; Duester, G.; Bamburg, J.R.
R.Adams, M.E., Minamido, L.S.; Duester, G.; Bamburg, J.R.
R.Adams, M.E., A14 7429, 1990
A.Tille: Nucleotide sequence and expression of a cDNA encoding chick brain actin depolym
A.Recession: A35702
A.Recession: A35702
A.Molcoule type: mRNA
A.Recession: A35702
A.Reces
destrin - pig
NATHernale names: actin depolymetiting lactor
C.Species: Sus serofa domestica (actestic pig)
C.Dudte to 3 Aug 1990 *sequence_revision us Aug 1994 *text_change become 2009
C.Dudte to 3 Aug 1990 *sequence_revision us Aug 1994 *text_change become 2009
C.Socossion: A35179
P.Mecryama, K.; Nishida, E.; Yopecawa, N.; Sakai, H.; Matsumoto, S.; Tida, K.; Yahara, J. Biol. Chem. 265, 5768-5773, 1990
A.Title: Destrin, a mammalian actin-depolymerizing protein, is closely related to collid A.Fefricone nable: A35179
A.Molecule type: mRNA
A.Residues: 1165 Augnst A.
A.Residues: 1165 Augnst A.
A.Residues: 1165 Augnst A.
A.Residues: 1165 Augnst A.
A.Residues: Astrone: brain
C.Comment Bestrin is an actin-binding protein that is capable of rapidly deperpment C.Superfamily: cofflin
C.Serpords: acetylated amino end, actin binding, phosphoprotein
C.Scrowords: acetylated amino end, actin binding predicted
C.Superfamily: acetylated amino end (Ala) (in mature form) *status predicted
F:2/Medified site acetylated amino end (Ala) (in mature form) *status predicted
F:2/Medified site acetylated amino end (Ala) (in mature form) *status predicted
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J. Cell Biol. 122, 623-533, 1993
A. Mittle. Isolation and characterization of a regulated form of actin depolymenizing fact
A. Reference number: A40672, Multi 93328764, PMID: 76.76,65
A. Molecula type: protein
A. Molecula type: protein
A. Molecula type: protein
A. Molecula type: J. S.; Bamburq, J.R.
R. Agnew, B.J.; Minamide, L.S.; Bamburq, J.R.
B. Agnew, B.J.; Minamide, L.S.; Bamburq, J.R.
A. Hitle. Feativation of plastery lated actin depolymenizing factor and identification of A. Reference number. A38989, MUD: 93340558, PMID: 7615564
A. Reference number. A389899, MUD: 93340558, PMID: 7615564
A. Contents: annotation acetylated amino end; phosphorylation site
C. Comment: Destiin is an actin-binding protein that is capable of rapidly depolymerizing
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A)Accession: A35703
A)Molecule type: mac.
A)Explainment of the type: MCCCO CR 192915, NID 9211092, PIDR AAA485711, PID:9211031
A)Experimental source: muscile
A)E
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Cell Biol. 122, 623-633, 1993
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100.0%; Pred. No. 1 46+02;
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Alcross-reterence TMR. 1225779, NIP-qF.4595, FIDN-AAAFORR9 1, F1E-q4-0958
A.Experimental source: strain Bangladesh 1975
E.Aguado, B., Scimes, E.P., Smith, G.L.
J. Gen. Virol. 73, 2887-2902, 1992
J. Gen. Virol. 73, 2887-2902, 1992
A.Tille. Nacleolide sequence of 21.8 kbp of variola major virus strain Harvey and com A.Reference number: 3Q1832; MUID:93057351; PMID:1331292
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A.Thibe Perental Viculesce determinants in terminal regions of variola smallpox vir A; Reference number 120488, MRD 9498747; PMID 9264798
                                                                                                                                                                                                                                                                                                   F.104 134/Region: actin binding *status predicted F.2/Mediffed site: acetylated amino end (Ala) (in mature form) *status experimental F.3/Binding site: phosphate (Ser) (covalent) *status experimental
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C.Species, Variola najor virus
C.Datc: 22 Get 1999 #scyprope_revision 22 Get+1999 #fext_change 21+151+2030
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A Residues: 1-168 cAOU-
A Cross-reforences TR XF 5-18 NIO 4518231, Film CAA4445.1, Film JF10232
A Experimental source: strain Harver
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F.15-34/Domain. transmembrane #status predicted :TMM>
F:133/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Regwords, acetylated amino end, actin binding, phosphoprotein
Epités/orodoct: destrin *status predicted AMA:
E.Zerio, Region, nuclear Loration signal
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Fred. No. 1.4e+02;
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A;Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RiJohnson, G.P.
subsiticted to Gerhank, June 1990
A.Refetence number, A33172
A.Recession: 142520
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Gaps

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A. Cross references. GR X69198: NII: 9456788; Plink: AA449662.1; PlIr: 9487032
A. Cross references. GR X69198: NII: 9456789; Plink: AA449662.1; PlIr: 9487032
A. Experimental source. strain. India-1967, ssp. major, isolate ind3
R. Kolykhalov, A. A.; Blincy, V. M.; Frolov, I.V.; Tolmenin, A.V.; Shchelkunov, S.N.; Sasubmilled to the EMBL Data Library, April 1992
A. Description. Nucleotide sequence analysis of the region of variola virus Xhol-E gen
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C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05 Nov-1999
C.Accession: 167436
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                    A.Accession. J01770
A.Mcheule type: DNA
A.Mcheule type: DNA
A.Mcheule type: DNA
A.Residues: 1-168 (-8M)-
A.Cross-references: DDHJ:D11079; NID:g222717; PIDM:HAA01806.1; PID:g222721
C.Keywords. 4]vobracteiu, Leaishembrane profein
F:1.36/Pomain: Signal sequence #status predicted <81G>
F:37.168/Product: SalL4R protein #status predicted <MT>
F:133/Hinding site: carbohydrate (Asn) (covalent) #status predicted
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A.Experimental source: strain India-1967, isolate ind3
C.Keywords: transmembrane protein
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100.0%; Pred. No. 1.46+02;
tive 0; Mismatches 0; Indels
     A:Peference number: JQ1757; MUID:91259063; PMID:2045793
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C; Date: 30-Sep-1943 #sequence_revision
C; Accession: B36852; $46864
R; Bllnov, V.M.
Submitted to GenBunk, November 1992
A; Reference number: A36859
A; Accession: B36852
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A37R protein – variola virus
N;Alternate names: A34R protein
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A;Accession: $46864
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-168 <KOL>
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Chartersion: T4420
Excression: T4420
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Example to the EMBL Data Library March 1907
Albest platon: T47420
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Albest platon: T47420
Albest pre-liminary: translated from CR/EMRL/PDR1
Albest dues: 1-168 CANTA
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Albertiption: Analysis of the complete coding sequence of DNA of alastrim variola minor A; Reference number: A72150
A. Arevession: C72168
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H.Smith, G.L.; Chan, Y.S.; Howard, S.F.
J. Gen. Virol. 72, 1349-1476, 1991
A.Tille: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right in
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C.Dale: 24-Nov-1999 #sagrence_revisios 24 Nov-1999 #fext_change 20 Jun 2000
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C:Dato: 30 Sep:1993 #sequence_revision 30 Sep:1993 #fext_change 20-Jun-2000
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A;Cross_references: GB:Y16780: NID-g5830555: PIDN-CAR54741 1; P1D-g5830702
     Selection
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                                                                                                                                                                                                                                                 A38R protein - variola minor virus (strain Garcia-1966)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salide profess precursor - vaccinia virus (strain WP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEV qlycoprotein - vaccinia virus (strain Ankara)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U94848; PIDN:AAB96529.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
  0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain Garcia-1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AjExperimental source: strain Ankara CjGeneties:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ouery Match
Hest Local Similarity 100.0
Free 5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: vaccinia virus
A;Variety: strain Ankara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                  C;Accession: C72168
                                                                                       59 KEELM 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 KEELM 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 KEELM 41
                                                 1 KEELM 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KEELM 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KEELM 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: MVA145R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: A38R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
T37420
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                       C72168
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Gaps

0; Query Match 100.0%; Score 24; DB 2; Length 182; Best Local Similarity 100.0%; Pred. No. 1.56+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

Search completed: January 16, 2003, 16:57:49 Job time : 10.2143 secs

